

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:26:53 : Search time 31.6762 Seconds
(without alignments)

2795.154 Million cell updates/sec

US-10-054-680-2

Perfect score: 4797

Sequence: 1 MAMLRLOPLTSAFLEHFLVY.....LWLLYLDFATLEAVCYIKGF 921

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*
1: plr1:*
2: plr2:*
3: plr3:*
4: plr4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3447.5	71.9	970	2 A36417	Na+/Ca2+-exchanger
2	3441	71.7	935	2 S43730	Na+/Ca2+-exchanger
3	3439.5	71.7	973	2 S32815	Na+/Ca2+-exchanger
4	3437.5	71.7	941	2 B53335	Na+/Ca2+-exchanger
5	3434.5	71.6	958	2 S32435	Na+/Ca2+-exchanger
6	3432.5	71.6	970	2 I48097	Na+/Ca2+-exchanger
7	3426	71.4	957	2 A53789	Na+/Ca2+-exchanger
8	3425.5	71.4	970	2 S27114	Na+/Ca2+-exchanger
9	3422	71.3	971	2 S28833	Na+/Ca2+-exchanger
10	3357	70.0	921	2 A54139	Na+/Ca2+-exchanger
11	2007	41.8	890	2 B89047	protein C10G8.5 [i
12	1192	24.8	807	2 T24110	hypothetical prote
13	659	13.7	152	2 I52640	cardiac sodium/cal
14	573.5	12.0	538	2 T00424	probable Na+/Ca2+
15	573	11.9	133	2 A48852	Na+/Ca2+-exchan
16	312	6.5	1199	2 S20969	Na+/Ca2+-K+-exchan
17	284.5	5.9	1014	2 T31433	Na+/Ca2+-K+-exchan
18	225	4.7	123	2 I46959	Na/Ca exchanger NA
19	215.5	4.5	591	2 T19746	hypothetical prote
20	205.5	4.3	1568	2 T08616	aggregation factor
21	201	4.2	4936	2 AH2515	hypothetical prote
22	190.5	4.0	2205	2 T08615	aggregation factor
23	170.5	3.6	611	2 T21747	hypothetical prote
24	169.5	3.5	3016	2 S77300	hypothetical prote
25	161	3.4	825	2 T08617	aggregation factor
26	150.5	3.1	591	2 S40705	hypothetical K+-exchan
27	147	3.0	590	2 S40707	hypothetical prote
28	144.5	3.0	703	2 T03888	Na+/Ca2+-K+-exchan
29	144	3.0	644	2 B96582	hypothetical prote

30	144	3.0	1428	2 AC2224	hypothetical prote
31	143.5	3.0	325	2 F65110	hypothetical 34.7
32	143	3.0	123	2 A53335	Na+/Ca2+-exchanger
33	142.5	3.0	325	2 C91138	hypothetical prote
34	142.5	3.0	325	2 F85983	hypothetical prote
35	142.5	3.0	1807	2 JC6319	integrin beta-4 ch
36	142	3.0	302	2 C64311	Na+/Ca2+-exchanger
37	141.5	2.9	318	2 G84196	cation antiporter
38	139.5	2.9	825	2 AB1841	hypothetical prote
39	139.5	2.9	1748	1 JN0786	integrin beta-4 ch
40	138	2.9	743	2 T38674	probable membrane
41	135.5	2.8	325	2 A10904	probable membrane
42	134	2.8	433	2 S74922	hypothetical prote
43	132	2.8	720	2 T02457	hypothetical prote
44	129.5	2.7	309	2 B72342	conserved hypothet
45	128.5	2.7	664	2 S66067	methionine-tRNA 11

ALIGNMENTS

RESULT 1

A36417 Na+/Ca2+-exchanging protein - dog

C:Species: Canis lupus familiaris (dog)

C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_Change 18-Aug-2000

C:Accession: A36417 R:Nicolli, D.A.; Longoni, S.; Philipson, K.D.

A:Title: Molecular cloning and functional expression of the cardiac sarcolemmal Na(+)

A:Reference number: A36417; MUID:91047958; PMID:1700476

A:Accession: A36417

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-970 <NCIC>

A:Cross-references: GB:M57523; NID:G164072; PIDN:AAA62766.1; PID:G164073; GB:M36119

C:Superfamily: human Na+/Ca2+-exchanging protein

C:Keywords: phosphoprotein; transmembrane protein

Query Match	71.9%	Score 3447.5;	DB 2;	Length 970;
Best Local Similarity	69.2%	Pred. No. 8.4e-224;		
Matches 677;	Conservative 109;	Mismatches 127;	Indels 65;	Gaps 10;
QY	1	MAMLRLOPLTSAFLEHFLVFLF--LNGLRNAGSGDVPSTGONNSCGSSDCKRGV	58	
DB	1	MLQLRLPFSMGCHLAVALLFSHVLDLSKTEMEBEGNETGE---CTGSIYCKRGV	56	
QY	59	ILPIVYPNPISLGDRIARIVYFVALIYMFGLVSIADRFMASIVITISOEREVTIKRPN	118	
DB	57	ILPIEPDPDPSFGDKIARATYFVAMVYMFGLVSIADRFMASIEVITISOEREVTIKRPN	116	
QY	119	GETSTTTIRWNETVSNLTLMALGSSAPDILLILEVCGHGFIAGDLGPSTVGSAAFPN	178	
DB	117	GETTQTVIRWNETVSNLTLMALGSSAPDILLILEVCGHGFIAGDLGPSTVGSAAFPN	176	
QY	179	FIITICVYVVPDGETRIKILRVFRTAAMSEFAYIMLMILAFAFGVGVYMGSLTL	238	
DB	177	FIILALCVYVVPDGETRIKILRVFRTAAMSEFAYIMLMILAFAFGVGVYMGSLTL	236	
QY	239	FFPFCVLLAVADRRLLFFYKTMHKKYRTDKRGIIIEGDPKPG---IEMDGKMNHS	295	
DB	237	FFPFCVLLAVADRRLLFFYKTMHKKYRTDKRGIIIEGDPKPG---IEMDGKMNHS	296	
QY	296	---FLDGNLVPLEGEVD---ESRREMIRLIKDKOKHPEKDLQVLVEMANYVALSHQO	348	
DB	297	VDFNFDGALV--LEVDERDODDEARREMARIRLIKELKOKHPEKDLQVLVEMANYVALSHQO	355	
QY	349	KSRATYRIQATPMATGAGNIILKKHAADAKKASSSEVHTDEPE--DFISKVFFDPCSYOC	407	
DB	356	KSRATYRIQATPMATGAGNIILKKHAADAKKASSSEVHTDEPE--DFISKVFFDPCSYOC	415	
QY	408	LENCAGVLLTVVRKGGDSKTYVDYKTEDEGSANAGADYEETEGVYVLPKGETOEFESVG	467	

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Db 416 LENCSTVALTIIRGGDLNTVVFVDFRTDEGTANAGSDYEFTEGVYFKRGFTOKETIRNG 475
Qy 468 IIDDIDFEDEHFEFVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVATVITLDDO 527
Db 476 IIDDIDFEDEENLHLNSNVKSSASEDGLIENHVS---ALACGSPSTAVITVIFDDO 532
Qy 528 HAGIFFECDTHVSSIGVMEYKVLRTSGARCTVYVPRFTVEGTAAGGGEDEFDTYGL 567
Db 533 HAGIFFECDTHVSSIGVMEYKVLRTSGARCTVYVPRFTVEGTAAGGGEDEFDTYGL 592
Qy 588 EFNNDVTYRKIVDEEYERQENFIALGEPKMEKNG----- 627
Db 593 EFNNDVTYRKIVDEEYERQENFIALGEPKMEKNG----- 652
Qy 628 -----ISDYTDK--LTMEEERKRIAEKGPVLEPKLEVI 663
Db 653 YGQPVKRYKVAHREPIRSTYITTAIEEYDQKPLTSKEEERRIAEKGRPLTSGHTYLEV 712
Qy 664 IEESYFEKTTVDKLIKTNLALVVGTHSWRQPMETVTSAGDEDEDESEBERLPSCED 723
Db 713 IEESYFEKTTVDKLIKTNLALVVGTHSWRQPMETVTSAGDEDEDESEBERLPSCED 772
Qy 724 YVNHFLTFVFKVLFACVPRPEYCHGACFRAVSLITIGMLTAITIGDLASHGCTIGLKDSY 783
Db 773 YVNHFLTFVFKVLFACVPRPEYCHGACFRAVSLITIGMLTAITIGDLASHGCTIGLKDSY 832
Qy 784 TAVVFAFGSVPTDFASKAALQDYADASIGNVTGSNAVNVEFLGIGLAWSAIATYMAL 843
Db 833 TAVVFAFGSVPTDFASKAALQDYADASIGNVTGSNAVNVEFLGIGLAWSAIATYMAL 892
Qy 844 QGQEFHVSAGTLAFSVLTFTFAFCISVLLYRRPHLGELGCGPRCKIATTWLVSLW 903
Db 893 NGQOFVSPPTLAFSVLTFTFAFCISVLLYRRPHLGELGCGPRCKIATTWLVSLW 952
Qy 904 LLYTFATLEAYCYIKGF 921
Db 953 LLYTFATLEAYCYIKGF 970

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RESULT 2
S43730
Na+/Ca2+-exchanging protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Aug-2000
C:Accession: S43730
R.Furman, I.; Cook, O.; Kasir, J.; Rahamimoff, H.
FEBS Lett. 319, 105-109, 1993
A:Title: Cloning of two isoforms of the rat brain Na(+)-Ca(2+) exchanger gene and their
A:Reference number: S32435; MUID:93202244; PMID:8454039
Accession: S43730
Status: preliminary
Molecule type: mRNA
A:Residues: 1-935 <FUR>
A:Cross-references: EMBL:X68812; NID:g288229; PIDN:CAAA48707.1; PID:g288230
C:Superfamily: human Na+/Ca2+-exchanging protein

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Query Match 71.7%; Score 3441; DB 2; Length 935;
Best Local Similarity 71.1%; Pred. No. 2, 2e-223;
Matches 673; Conservative 109; Mismatches 123; Indels 42; Gaps 11;

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Qy 4 LRLQPLTSAFLHGLVTFVFL-----NGLRARAGSGDVPSTGQNNESGSGSDCK 55
Db 2 LRLSPLTSMGRLVTLVLAFTVHDHTADAEAGGNN-----ETTECTGSGYCK 53
Qy 56 EGVILPWPENSLDKTARVIVFVALVLMFVSIADRMASTEVTSQREVTYK 115
Db 54 KGVILPWPENSLDKTARVIVFVALVLMFVSIADRMASTEVTSQREVTYK 113
Qy 116 KPNGETSTTIRVWNETVSNLTALAGSSAPETILSLIEYCGHGTAGDGPSTIVGSA 175
Db 114 KPNGETSTTIRVWNETVSNLTALAGSSAPETILSLIEYCGHGTAGDGPSTIVGSA 173
Qy 176 ENMFIITGICVYVDPGETRKIKHLRVFTTAAMSIFAYITWILAVFSPGVVQWEG 235

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Db 174 ENMFIITGICVYVDPGETRKIKHLRVFTTAAMSIFAYITWILAVFSPGVVQWEG 233
Qy 236 LTFEFPVVCVLAADVADKRLTFKYMKKKYRTDKHNGIILETGDPHK---IEMDKMM 292
Db 234 LTFEFPVVCVLAADVADKRLTFKYMKKKYRTDKHNGIILETGDPHK---IEMDKMM 293
Qy 293 NSH---FLDGNLVLPEKEDV---ESRREMRILDKLQKHPKEDLDQVEMANYALS 345
Db 294 NSHVDNFDLQALV-LEVDERDQDDEARREMAIILKELQKHPKEDLDQVEMANYALS 352
Qy 346 HQKSAFRIQATRMATGAGNITLKKHAADQAKKASMSNVHDEDE-DEISVFEFPCS 404
Db 353 HQKSAFRIQATRMATGAGNITLKKHAADQAKKASMSNVHDEDE-DEISVFEFPCS 412
Qy 405 YQLENCGAVLTLVVRKSGMSKTMVYDKTEDGSAANAGADYEFTEGVTLKRGFEOKPE 464
Db 413 YQLENCGAVLTLVVRKSGMSKTMVYDKTEDGSAANAGADYEFTEGVTLKRGFEOKPE 472
Qy 465 SVGIIDDIDFEDEHFEFVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVATV 523
Db 473 SVGIIDDIDFEDEHFEFVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVATV 528
Qy 524 LDDDHAGITFECDTHVSSIGVMEYKVLRTSGARCTVYVPRFTVEGTAAGGGEDEFDT 583
Db 529 LDDDHAGITFECDTHVSSIGVMEYKVLRTSGARCTVYVPRFTVEGTAAGGGEDEFDT 588
Qy 584 YGELEKNDVETVTKIVKIVDEEYERQENFIALGEPKME-----RGISDYTD-----R 634
Db 589 YGELEKNDVETVTKIVKIVDEEYERQENFIALGEPKME-----RGISDYTD-----R 648
Qy 635 KLTMEERKRIAEKMPVLEPKLEVIIEESYFEKTTVDKLIKTNLALVVGTHSWR 694
Db 649 KLTMEERKRIAEKMPVLEPKLEVIIEESYFEKTTVDKLIKTNLALVVGTHSWR 708
Qy 695 QFMEATTVSAGDEDEDESEBERLPSCFDYMFLVFMKVLFAFVPTLEYMGMACTV 754
Db 709 QFMEATTVSAGDEDEDESEBERLPSCFDYMFLVFMKVLFAFVPTLEYMGMACTV 768
Qy 755 SILIIGMLTAITIGDLASHGCTIGLKDSYAVVFAFGTSVPTDFASKAALQDYADAS 814
Db 769 SILIIGMLTAITIGDLASHGCTIGLKDSYAVVFAFGTSVPTDFASKAALQDYADAS 828
Qy 815 IGWVTSNAVNVEFLGIGLAWSAIATYMALQGEFHVSACTLAFSVLTFTFAFCISV 874
Db 829 IGWVTSNAVNVEFLGIGLAWSAIATYMALQGEFHVSACTLAFSVLTFTFAFCISV 888
Qy 875 YRRRPHLGELGCGPRCKIATTWLVSLWLTLYTFATLEAYCYIKGF 921
Db 889 YRRRPHLGELGCGPRCKIATTWLVSLWLTLYTFATLEAYCYIKGF 935

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RESULT 3
S32815
Na+/Ca2+-exchanging protein - human
N:Alternate names: Na+/Ca2+ antiporter; Na+/Ca2+ exchanger
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000
C:Accession: S32815; A56767
R.Komuro, I.; Menniger, K.E.; Philipson, K.D.; Izumo, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 4769-4773, 1992
A:Title: Molecular cloning and characterization of the human cardiac Na(+)/Ca(2+) exc
A:Reference number: S32815; MUID:92263251; PMID:1374913
Accession: S32815
Status: preliminary
Molecule type: mRNA
A:Residues: 1-973 <IZU>
A:Cross-references: EMBL:M91368; NID:g180672; PIDN:AAA35702.1; PID:g180673
R. Oufuji, P.; Hadley, R.W.; Kieval, R.S.; Lederer, W.J.; Schulze, D.H.
Am. J. Physiol. 263, C1241-C1249, 1992
A:Title: Expression of the Na-Ca exchanger in diverse tissues: a study using the clon
A:Reference number: A56767; MUID:93118744; PMID:1476165
Accession: A56767

```

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 4-253, 'K', 255-627, 'K', 629-692, 'K', 694-973 <KOF>
A:Note: sequence extracted from NCBI backbone (NCBI:121276, NCBI:121277)
C:Superfamily: human Na+/Ca2+-exchanging protein
C:Keywords: cardiac muscle; heart; phosphoprotein; transmembrane protein

Query Match 71.7%: Score 3439.5; DB 2; Length 973;
Best Local Similarity 68.9%; Pred. No. 2.9e-223;
Matches 674; Conservative 111; Mismatches 128; Indels 65; Gaps 10;

```
1 MAWLRLQPLTSAPLHGLVTVLF--LNGLRAGAGSGDVPSTGONNCSGSSDCKEGV 58
4 MRRSLSPFMSMGHLLVTVSLFSHDVIAEREMEGENGE-----CTGSYCKKGV 59
59 ILPIWENPSLGDKIAIVYVVALIYMLGVSIIADREMAIEVITSOERETIKPN 118
60 ILPIWENPSLGDKIAIVYVVALIYMLGVSIIADREMAIEVITSOERETIKPN 119
119 GEMSTTIRVWNETVSNLTLALGSSAPETLSIEVCGHGFAGDGLGPTIVGSAFNM 178
120 GETTKTVRIWNETVSNLTLALGSSAPETLSIEVCGHGFAGDGLGPTIVGSAFNM 179
179 FIIGICVYVDPGETRIKILRVFITAAMSIKAYIMLILAFSPGVVQVWEGLLTL 238
180 FIILALCVYVDPGETRIKILRVFITAAMSIKAYIMLILAFSPGVVQVWEGLLTL 239
239 FEPFVCLLVAVADKRLLYKVMHKYRTDKHNGIITIEGDHPK--IEMDKMNSH 295
240 FEPFVCLLVAVADKRLLYKVMHKYRTDKHNGIITIEGDHPK--IEMDKMNSH 299
296 ---FLDGNLVPLEGEVD---ESRREMIRILKOKHPEKIDOLVEMANYALSHQ 348
300 VENLIDALV--LEVDERDQDDEARREMARILKOKHPEKIDOLVEMANYALSHQ 358
349 KSRAFYIQTATRMKTGAGNLIKHAEOAKKASSMEVHTDEPE-DFISKVFPDSC 407
359 KSRAFYIQTATRMKTGAGNLIKHAEOAKKASSMEVHTDEPE-DFISKVFPDSC 418
408 LENCAGVLLTVVRKGDMSKTMVVDYKTEGDSANAGADYEFTGVLLKPGETKES 467
419 LENCAGVLLTVVRKGDMSKTMVVDYKTEGDSANAGADYEFTGVLLKPGETKES 478
468 IIDDIDIEEDHFFVRLSNVRIEEOPEEGMPRAIFNSLPLRAVLASPCATVYI 527
479 IIDDIDIEEDHFFVRLSNVRIEEOPEEGMPRAIFNSLPLRAVLASPCATVYI 535
528 HAGIIFTECDTIHVESISIGVMEVYLRTSGARTVIVPRTVEGTAKGGEDFET 587
536 HAGIIFTECDTIHVESISIGVMEVYLRTSGARTVIVPRTVEGTAKGGEDFET 595
588 EFKNDEVTAKITRKYVDEEYEROEENFIALGEPKMMERG----- 627
596 EFQNDIEVITKIVYIDDEEYEROEENFIALGEPKMMERG----- 655
628 -----ISDVDRK--LMEEEEARIAEMGPRVVGEPHKLVI 663
656 FGQVFRKVAAREHPIISTVITTIADYDDKPLTSKEEERRIEMGRPLIGEHKLE 715
664 IEESYERKTVDKLIKTNLNLVGTSHMRQOFMEATVISAAGDEDESEERLPSCF 723
716 IEESYERKTVDKLIKTNLNLVGTSHMRQOFMEATVISAAGDEDESEERLPSCF 775
724 YVMHFLTVFKVLFACVPTPEYCHGMACFAVSILIGMLTAIIGDLASHFECT 783
776 YVMHFLTVFKVLFACVPTPEYCHGMACFAVSILIGMLTAIIGDLASHFECT 835
784 TAVAFVAFGSTVPTPAKAAADYVADASIGVNTGSNANVFLGIGLASVAIYAL 843
836 TAVAFVAFGSTVPTPAKAAADYVADASIGVNTGSNANVFLGIGLASVAIYAL 895
844 OGQEFHVSAGTLASFVTLFTTFAFVCSVLLYRRRPHLGELGPRGCKLTTWLV 903
```

Db 896 NGEQKVSFGTLASFVTLFTTFAFVCSVLLYRRRPHLGELGPRGCKLTTWLV 955
QY 904 LLYLFATLFAKCYIKGF 921
Db 956 LLYLFATLFAKCYIKGF 973

RESULT 4

B53335
Na+/Ca2+-exchanging protein NCX1, splice form NACA6 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Aug-2000
C:Accession: B53335
R:Kofuji, P., Lederer, W.J., Schulze, D.H.
J. Biol. Chem. 269, 5145-5149, 1994
A:Title: Mutually exclusive and cassette exons underlie alternatively spliced isoform
A:Reference number: A53335; MUID:94148976; PMID:8106495
A:Accession: B53335
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-941 <KOF>
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBI:144050)
C:Superfamily: human Na+/Ca2+-exchanging protein

Query Match 71.7%: Score 3437.5; DB 2; Length 941;
Best Local Similarity 71.0%; Pred. No. 3.8e-223;
Matches 669; Conservative 111; Mismatches 125; Indels 37; Gaps 11;

```
8 PLTSAFLHFGVTVTVLF--LNGLRAGAGSGDVPSTGONNCSGSSDCKEGVLP 66
9 PFSMGHLLALVALFFRVVDHVSATEMEGEGNTE-----CTGSYCKKGVLP 64
67 NPSLGDKIAIVYVVALIYMLGVSIIADREMAIEVITSOERETIKPNGETST 126
65 DPSGDKIARATVYFVAVMYMFLGVSIIADREMAIEVITSOERETIKPNGET 123
127 RVNNETVSNLTLALGSSAPETLSIEVCGHGFAGDGLGPTIVGSAFNMFIIG 186
124 RVNNETVSNLTLALGSSAPETLSIEVCGHGFAGDGLGPTIVGSAFNMFIIG 183
187 VYIDPGETRIKILRVFITAAMSIKAYIMLILAFSPGVVQVWEGLLTLFEP 246
184 YVDEGETRIKILRVFITAAMSIKAYIMLILAFSPGVVQVWEGLLTLFEP 243
247 LAMVADKRLLYKVMHKYRTDKHNGIITIEGDHPK--IEMDKMNSH---FL 300
244 FAWVADKRLLYKVMHKYRTDKHNGIITIEGDHPK--IEMDKMNSH---FL 303
301 LVPLEGEVD---ESRREMIRILKOKHPEKIDOLVEMANYALSHOOKSRAFY 356
304 LVPLEGEVD---ESRREMIRILKOKHPEKIDOLVEMANYALSHOOKSRAFY 362
357 QATRMKTGAGNLIKHAEOAKKASSMEVHTDEPE-DFISKVFPDSCYOCL 415
363 QATRMKTGAGNLIKHAEOAKKASSMEVHTDEPE-DFISKVFPDSCYOCL 422
416 LTVVRKGDMSKTMVVDYKTEGDSANAGADYEFTGVLLKPGETKESVGI 475
423 LTVVRKGDMSKTMVVDYKTEGDSANAGADYEFTGVLLKPGETKESVGI 482
476 EDEHFFVLSNVRILEEEOPEEGMPRAIFNSLPLRAVLASPCATVYI 535
483 EDEHFFVLSNVRILEEEOPEEGMPRAIFNSLPLRAVLASPCATVYI 539
536 CDTHVSESIGVMEVYLRTSGARTVIVPRTVEGTAKGGEDFETVYGELEFN 595
540 ESVTHVSESIGVMEVYLRTSGARTVIVPRTVEGTAKGGEDFETVYGELEFN 599
596 KTIKRVYIDDEEYEROEENFIALGEPKMMERG-----ISDVDRK--L 639
600 KTIKRVYIDDEEYEROEENFIALGEPKMMERG-----ISDVDRK--L 659
```


Db 177 FIIALCVYVPOSEETKIKHLNLFVETLAMSIFATLWLTLLSVLSRQVYEWMEGLTF 236
 239 FEPVVCVLLANVADKRLLFYKYNMKYKTRDKNRGIIETEGDPKG---IEMDGKMNSH 295
 Db 237 FEPFICVFAVAVADRLLLFYKYVYKRYRAGQKGMIIIEHEDGRPSKTEIEMDKQVNVSH 296
 296 ---FLDGNLVPLEKEVD---ESRREMRILDKLQKRPEDLDQVEMANYTALSQQ 348
 Db 297 VENFLDGLV-LVEYDEADODDEEARREMAILKELQKRPHEKEIRDLIELAYQLVSQQ 355
 349 KSRAFYRLQATRMGTAGNLKKHAEOAKKASMSVEYTDPER-DEISKVPEDDCSQC 407
 Db 356 KSRAFYRLQATRLMTGKGNLKKRAADQARKAVSHMEVTEVAENDVPYSKIFPDGTYQC 415
 408 LENCQAVLLTVVRKKGDMSKTMVVDYKTEBDGSANAGADEFEETGYVVLKPGETOKEFSVG 467
 Db 416 LENCQVALLTIIRRGDGLTNTVEYDFPTEBDGTANAGSDYEFEGTVVFPKGTOKEINVG 475
 468 IIDDIDFEEDHEFVRLSNVRIEEOPEBGMPAITNSLPRLAVLASPCVATVILDD 527
 Db 476 IIDDIDFEEDENFLVHLSNKKVSSSEASDGLTANHIS---TLACGSSTVATVIFPDD 532
 528 HAGIFTPECOTIHVSESIGVMEVKVLRTSARGCTVVPRTVEGRAGKGGEFETTVEL 587
 Db 533 HAGIFTPEEPVTHSESIGVMEVKVLRTSARGCNVTVPKTIEGTARGGGEDFETTGEL 592
 588 EFKNDETIVKTRVNIYDEEYERQENEFIALGEPKMERG----- 627
 Db 593 EFNODEIVKITSVAVIDDEYEKNNKFFLEIGSRVLEKSEKALLNLNGFTTGGHL 652
 628 -----ISDVTDRK--LTMEEBEAKRIAEKRPVLEHPRKLEVI 663
 Db 653 YGQGVLRKVRHARDPIRSTVITTADEDDKOPLTSEEEERRIAEIGRPIIGEHRTKLEVI 712
 664 IEESYERTYVDKILKTNIALVNGTSHMDDQMEALITYSAGCDDDEDESGERLRPSCFD 723
 Db 713 IEESYERTYVDKILKTNIALVNGTSHMDDQMEALITYSAGCDDDEDESGERLRPSCFD 772
 724 YVMHFLTVFMKVLFCVPTPEYCHGNACFAVSLIILGMLTAIIGDLSHFCTIGLKDQSV 783
 Db 773 YVMHFLTVFMKVLFCVPTPEYCHGNACFAVSLIILGMLTAIIGDLSHFCTIGLKDQSV 832
 784 TAVVFAVAGTSVPDTFASKAALQDYYADASIGNVTGSNAVNVFLGIGLMSVAIYAL 843
 Db 832 TAVVFAVAGTSVPDTFASKAALQDYYADASIGNVTGSNAVNVFLGIGLMSVAIYAL 892
 844 OGQGFHVSAGTLAFSVLFTIIFAPVCISVLLYRRRHLDGELGGRGCKLATIWLFSVLM 903
 Db 893 NGQGFHVSAGTLAFSVLFTIIFAPVCISVLLYRRRHLDGELGGRGCKLATIWLFSVLM 952
 904 LLYLFAFLTEAYCYIKGF 921
 Db 953 LLYLFAFLTEAYCYIKGF 970

RESULT 7
 A:53789
 Na/Ca2+-exchanging protein precursor, splice form NACA7 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 18-Aug-2000
 C:Accession: A53789; JX0288
 R:Lee, S.L.; Yu, A.S.L.; Lytton, J.
 J: Biol. Chem. 269, 14849-14852, 1994
 A:Title: Tissue-specific expression of Na(+)-Ca2+ exchanger isoforms.
 A:Reference number: A53789; MIMD:94253030; PMID:8195112
 A:Accession: A53789
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-957 <LE>
 R:Nakaseki, Y.; Iwanoto, T.; Hanada, H.; Imagawa, T.; Shigetawa, M.
 J. Biochem. 114, 528-534, 1993

A>Title: Cloning of the rat aortic smooth muscle Na⁺/Ca²⁺ exchanger and tissue-specific
 A:Reference number: JX0288; MUID:94103175; PMID:8276763
 A:Accession: JX0288
 A:Molecule type: mRNA
 A:Residues: 1-957 (NAK>
 A:Experimental source: aortic smooth muscle
 C:Superfamily: human Na⁺/Ca²⁺-exchanging protein
 C:Keywords: Ion transport; membrane protein
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:33-957/Product: Na⁺/Ca²⁺ exchanger #status predicted <NAT>

Query Match 71.4% Score 3426; DB 2; Length 957;
 Best Local Similarity 69.6% Pred. No. 2,3e-22;
 Matches 674; Conservative 105; Mismatches 126; Indels 64; Gaps 11;

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4  LRLQLTSAFLHFGCIVTFLF-----NGLRAGSGSDVPTSGNNESGSSDCK 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  2  LRLSLPWNYSKQFLVTLVALLFTVHDITADTLEETGNN-----ETTECGSYCK 53

Qy  56  EGVILPIWPNPNSLGDKIARVIVYFVALIYFGLVSIIDRFMASIEVITTSQREVTIK 115
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  54  KGVILPIWEPQSPSGDKIARVIVYFVALIYFGLVSIIDRFMASIEVITTSQREVTIK 113

Qy  116  KNGETSTTTIRVNWETYSNLTLMALGSSAPBILLSLEVCGHGFIAGDLDPSTIVSAA 175
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  114  KNGETSTTTVIRINWETYSNLTLMALGSSAPBILLSLEVCGHGFIAGDLDPSTIVSAA 173

Qy  176  FMMFIIIGICVIVPDGERTKIKHLRVFEITAAANSIFAYILYMLIAVFSQVQVWEG 235
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  174  FMMFIIIALCVIVPDGERTKIKHLRVFVFLAANSIFAYITLIIYLSVSSGCVIEWEGL 233

Qy  236  LTLFFPVCVLLAWVADRLLLFYKYMHKKYRTDKHGIITIEGDHPKG---IEMDGKM 292
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  234  LTFEFPICVAFWAVADRLLLFYKYVYKRYRAGKRGMIIEHGDGRASKTEIEMDGKV 293

Qy  293  NSH---FLDGNLIVPLEGEVD---ESRREMITIKLKKHPEKDLQVEMANYALS 345
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  294  NSHVNDFLDGALV-LEVERDQDDEARREARILIKELKQHNPKIEQLITELANVOLS 352

Qy  346  HOOKRAFYRIQATPMYTGAGNLIKLNAAEQAKKASSSEVHTDPE--DFISKYFPDPS 404
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  353  QOOKRAFYRIQATPLMTGAGNLIKLNAAADAKRAVSHNEVMDVENDPYSKYFEEGCT 412

Qy  405  YQCLENGCAVLLTVYRKGDMSKTYVDYKTEDGSANAGADYEETEGTVLKPGETQKEF 464
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  413  YQCLENGCAVALLTIRRGSLDLNTVFDPFRLEDGPAANGSDYEETEGVIAKPEGTQKEI 472

Qy  465  SVGIIDDDIFEEDEHFYRLSNVRIEEQPEBGMPIAFNSLP.LPR-AVLAPCVAVTYI 523
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  473  RVGIIIDDDIFEEDEHFLVLSNVRVSSEVSBDG----TLDNHNYSALACLSPTATYTI 528

Qy  524  LDDHAGIIFTEFCDDIHYSESIGVMEVYVLTSGARGVVIYPPFTVEGTAGGDEDEDT 583
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  529  FDDHAGIIFTEEPYTHSESIGIMEVYVLTSGARGVVIYPTTIEGTAGGDEDEDT 588

Qy  584  YGELEFKNDEYKTIKRVIVDEEYERQENFIALGPKKMERG----- 627
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  589  CGELEFQNDYEIKITITIPREYERKESQSYLVEERKPIRGMKGKGFITLGPVPRKV 646

Qy  628  -----ISDVYDKR-LTMEEBEAKRIAEMKPVLGHPKILEVITIESEYERKT 672
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  649  HARHPIRSTVISISEEDDKQPLTSKEEERRIAEMGRPIILGHTKLEVIIESEYERKS 708

Qy  673  TVYDKIKTKTNIALVYGTSMRQDQMEATTVSAAGDEDEDEGEERLPSCPVYVHFLTVF 732
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  709  TVYDKIKTKTNIALVYGTSMRQDQMEATTVSAAGDEDDDEGEERLPSCPVYVHFLTVF 766

Qy  733  WKVLEACVPTEYCHGMAFCFAVSIILIGMLAIIGDLASHGCGTIGLKDSTAVAVFAFG 792
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  769  WKVLEAFAPPTPEYNGMAFCFVSIILMIGLLAFLIGDLASHGCGTIGLKDSTAVAVFAFG 828

Qy  793  TSVPTFASKAALADQVYADASIGNVTGSNAVNVFLIGLIGLAVAAIYMALQGEFHVA 852
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
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Db      829 TSVPTFASKVAATGDOQADASIGAVTGSNAVNVFLGIVGAMSIATYHAANGDEQFKVSP 888
Oy      853 GTLASFVLTFTFAFVCIISVLLYRRRPHLGEELGEPGRCCKATTWLFVSLMILYTLFATL 912
Db      889 GTLASFVLTFTFAFVCIISVLLYRRRPHLGEELGEPGRCCKATTWLFVSLMILYTLFATL 948
Oy      913 EAYCYIKGF 921
Db      949 EAYCHIKGF 957

RESULT 8
S27114
Na+/Ca2+-exchanging protein precursor, cardiac - bovine
N:Alternate names: Na+/Ca2+ antiporter
C:Species: Bos primigenius taurus (cattle)
C:Date: 22-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 18-Aug-2000
C:Accession: S27114; S18388
R:Accession: J.F.: Condrescu, M.; Kroupis, C.; Nelson, H.; Nelson, N.; Nicoll, D.; Philipson
Arch: Biochem. Biophys. 298, 553-560, 1992
Artile: Cloning and expression of the bovine cardiac sodium-calcium exchanger.
Reference number: S27114; MUID:93037494; PMID:1416984
Accession: S27114
A:Molecule type: mRNA
A:Residues: 1-970 <ACCE>
A:Cross-references: GB:I06438; NID:g163033; PIDN:AAA30509.1; PID:g163034
R:Dutkin, J.T.; Ahrens, D.C.; Pan, Y.C.E.; Reeves, J.P.
Arch. Biochem. Biophys. 290, 369-375, 1991
Artile: Purification and amino-terminal sequence of the bovine cardiac sodium-calcium
A:Reference number: S18388; MUID:92027750; PMID:1929404
Accession: S18388
A:Molecule type: protein
A:Residues: 33-40, 'X', 42-44 <DUB>
A:Experimental source: heart
C:Superfamily: human Na+/Ca2+-exchanging protein
C:Keywords: cardiac muscle; heart; ion transport; membrane protein
F.1-32/Domain: signal sequence #status predicted <SIG>
F.33-97/Product: Na+/Ca2+ exchange protein, cardiac #status predicted <MAT>

Query Match      71.4%; Score 3425.5; DB 2; Length 970;
Best Local Similarity 68.7%; Pred. No. 2,5e+22;
Matches 672; Conservative 110; Mismatches 131; Indels 65; Gaps 10;

Oy      1 MAMLMLOPLTSFLHFGLVTLF--LNGLRRAEGSGSDVSTGQNNSSCSSCKCKGV 58
Db      1 MLOFSLPTLSGFLVAVMALFESHVDHISAEITMBEGBGNETG---CTGSIYCKGKV 56
Oy      59 ILPIYVPEPNSGKDIARIYVVALIYMFGLVSIIDARFMAISIVITISOEREVITKKN 118
Db      57 ILPIEPPDPSGDKIARIATYVFVAMVMEFLGVSIIADRFMSIEVITISOEREVITKKN 116
Oy      119 GETSTTTIRWNEVTSNLTLMALGSSAPEILSLIEVCGHGFIAGDLGPSTIVGSAENM 178
Db      117 GETTETVIRVINEYTSNLTLMALGSSAPEILSLIEVCGHNETAGDLGPSTIVGSAENM 176
Oy      179 FTIIICGVYVPRDGETRIKHLRVFETIAMSIFKYLMLMIAFSGGVQVQWEGGLTL 238
Db      177 FTIIALGVYVPRDGETRIKHLRVFETIAMSIFKYLMLIYILSVSSGVVEVWEGGLTL 236
Oy      239 FFFPVCLVLAWADRRLLFFYKYMKKKYRTDKHGIIEEGDHPKG---IEADGKMNSH 295
Db      237 FFFPLCVFAWVADRRLLFFYKYVYKRYRAGKORGIIEHEDGRPSKTEIEDGKVYVSH 296
Oy      296 ---FLDGNLVLPLEGKVD---ESRREMIKILDKLQKHPKEDLDQVEMANYALSHQ 348
Db      297 VDSFLDGLV--LEVDERDQDDDEARREMARILKELQKHPKEITQLLELANYQLSQQ 355
Oy      349 KSRAFYRIQATRMATGAGNIIKKHAEDAKKASSSEVYHTEDEP--DFTISKYFEDPCSTQC 407
Db      356 KSRAFYRIQATRMATGAGNIIKKHAEDAKKASSSEVYHTEDEP--DFTISKYFEDPCSTQC 415
Oy      408 LENCVAVLLTVYRKRGDSKMTYVYVYKTEEDGSANNGADYETTEGVVULKPEIQKEFSVG 467
Db      408 LENCVAVLLTVYRKRGDSKMTYVYVYKTEEDGSANNGADYETTEGVVULKPEIQKEFSVG 467

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Db 416 LEMTVALTLIIRRGGLDITNVFVDFERTEDGTANAGSDYEFTEGTVFKPEGTOKEIRVG 475

Qy 468 IIDDIDFEEDHFFVRLSNVRIEEOPEGMPPALFNSLPRLPRAVLASPCATATITLDDO 527

Db 476 IIDDIDFEEDENFVLHNSNVKVSLEASDGIIEASHVS--TLACLSPSTATYITPDDO 532

Qy 528 HAGIETFECDITIHVSESIIGVMEVVLRTSGARGVIVYFERTVEGAAGGSDFDFTGEL 587

Db 533 HAGIETFECPVTHVSESIIGVMEVVLRTSGARGVIVYFERTVEGAAGGSDFDFTGEL 592

Qy 588 EFKNDYETKTRVKIVIDEEEXEROENFEIALGEPKRMERG----- 627

Db 593 EFONDEIYKTIISVYVIDEEYKNNKTFLEIGDEPRIVEMSEKALLINELGFTITGKL 652

Qy 628 -----ISDYDRK--LMEEBEAKRIAMKRPVLGEMPKLEVI 663

Db 653 YGQPVFRKVAREHPLPSTIITITIADEYDDOKPLTSCSEEBERRIAMGNPPIIGERTLEVI 712

Qy 664 IEESYEFKTYADKLIKKNLALVYGTSHMRQOFMEATIVSAAGDEDESGEERLPSCFD 723

Db 713 IEESTEEFSTYDKLIKKNLALVYGTSHMRQOFMEATIVSAAGDEDESGEERLPSCFD 772

Qy 724 YVMHFLVYFWKVLVFAQVDPTEYCHGMACFAVSIILIGMLTAIIGDLSAHFSGITGLDSV 783

Db 773 YVMHFLVYFWKVLVFAQVDPTEYCHGMACFAVSIILIGMLTAIIGDLSAHFSGITGLDSV 832

Qy 784 TAVYFVAGTSVPDTFASKAALODVADASIGVATGNSANVNLGIGLANSVAATYVAL 843

Db 833 TAVYFVAGTSVPDTFASKAALODVADASIGVATGNSANVNLGIGLANSVAATYVAL 892

Qy 844 OGOEYFVAGTSVPDTFASKAALODVADASIGVATGNSANVNLGIGLANSVAATYVAL 903

Db 893 NGEOKFVAGTSVPDTFASKAALODVADASIGVATGNSANVNLGIGLANSVAATYVAL 952

Qy 904 LLYILFATLEAVCYIKGF 921

Db 953 LLYIFSSLEAVCHIKGF 970

RESULT 9

S28833

Na+/Ca2+-exchanging protein - rat

N.Alternate names: Na+/Ca2+ antiporter; Na+/Ca2+ exchanger

C.Species: Rattus norvegicus (Norway rat)

C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000

C.Accession: S28833; S25552

R.Low, W.; Kasir, J.; Rahamimoff, H.

FEBS Lett. 316, 63-67, 1993

A.Title: Cloning of the rat heart Na(+)-Ca(2+) exchanger and its functional expression

A.Reference number: S28833; MUID:93138118; PMID:8422940

A.Accession: S28833

A.Molecule type: mRNA

A.Residues: 1-971 <LOW>

A.Cross-references: EMBL:X68191; NID:957208; PIDN:CAA8273.1; PID:957209

R.Low, W.; Kasir, J.; Boulter, J.; Heinemann, S.; Rahamimoff, H.

submitted to the EMBL Data Library, August 1992

A.Reference number: S25552

A.Accession: S25552

A.Molecule type: mRNA

A.Residues: 1-194, 'F', 196-971 <LO2>

A.Cross-references: EMBL:X68191

C.Superfamily: human Na+/Ca2+-exchanging protein

C.Keywords: ion transport; membrane protein; phosphoprotein

Query Match 71.3%; Score 3422; DB 2; Length 971;

Best Local Similarity 68.6%; Pred. No. 4,4e-222;

Matches 674; Conservative 106; Mismatches 125; Indels 78; Gaps 11;

Qy 4 LRLQPLTSAFLHFGIVTFVLF-----NGLRAEAGSGSDVSTGQNNESCGSSDCK 55

Db 2 LRLSLPNTVSGFRVLTVLALLFTVHDIHTADTAEATGCGN-----ETTEGSGSYCK 53

Qy 56 EGVILPITVPEPNSIGDKIARIVYFVALIIMFGLSVSIADRPASILEVITISQREVTIK 115

Db 54 KGVLLPIHEPQDPSPGDKIARATYFVAAMVYFELGVSIIADRFMSSEIVTISQEKRIITIK 113
Oy 116 KPNGETSTTTIVMNETYSNLTLMALGSSAPILLSLIEVCGHGFACGLGPGSTTVGSA 175
Db 114 KPNGETTTTIVMNETYSNLTLMALGSSAPILLSLIEVCGHGFACGLGPGSTTVGSA 173
Oy 176 FMFPIIGICVVIDGGERIKHLRVFPIITAMSSIFATIMLYMLTAVSPGVOWEGL 235
Db 174 FMFPIIALCYVVPDGETRIKHLRVFPIITAMSSIFATIMLYMLTAVSPGVOWEGL 233
Oy 236 LTFEPFVOLLAMADKRLTFYKMHKKYRTDKHGIIEETEGDHPKQ---IEMDGKMA 292
Db 234 LTFEPFICVFAVMAARLTFYKYKRYRAGQKGMILIEHGDPRPAKTEIEMDGKAV 293
Oy 293 NSH---FLDGNLVLEGGKVD---ESRREMRILKDLKQKHPKEDLDLVEMANYALS 345
Db 294 NSHVNFLDGNLV---LEVERDODDEDEARERMARILKELQKHPKEDLIELANYQVLS 352
Oy 346 HQKRAFRIOATMMTGAGNLLKKAHAEQAKKASMEVHTDEPE-DFISKVPFDPGS 404
Db 353 QOQKRAFRIOATRLMTAGNLLKRAHADQAKKASMEVMDVDVENDAVSKVFEQGT 412
Oy 405 YOCLENCGAVLLTVYRKGGDSKTMVDYKTEGDSANAGADYEETEGTVLKPGETQKEF 464
Db 413 YOCLENCGVALTLIRRGDLTNVFPVDRTEGDTANAGSDVEFTGTYIFKPGETQKEI 472
Oy 465 SVGIIDDDIFEEDEHFYRLSNVRIEEOPEEGMPALFNSPLPR-AVLASPCVATVTI 523
Db 473 RGIIDDDIFEEDEHFNVLHNSVRVSEVSEDEG---IIDSNHVSAIACLGSPNATITRI 528
Oy 524 LDDHAGITFECDTIHVESIGVMEVKVLRSGAGTVTFPRFVEGAKSGGEDEFT 583
Db 529 FDDHAGITFEPEPTTHSESIGIMEVKVLRSGAGNVILTYKITEGARSGGEDEFT 588
Oy 584 YGELEFKNDETVKTRVKIVDEEYERQENFIALGEPKMER----- 626
Db 589 CSELEFQNDIEIKTISVKYVIDEYKKNFTFIEIGEPLVEMSEKKALLNBLGFTLT 648
Oy 627 -----GISDVTRK--LTMEDEBKRIAEKGRPVLGHP 658
Db 649 ECKKMYGQVPRKVARHARPIRPTVYISISEYDDKQPLSKSEEEERIRIEMKRPILIGERT 708
Oy 659 KLEVIIEESYEFKTVDKLIKTNLALVYTHSMRQDEMEATVTSAAGEDDESEGERL 718
Db 709 KLEVIIEESYEFKTVDKLIKTNLALVYTHSMRQDEMEATVTSAAGEDDESEGERL 768
Oy 719 PSCFDYVMHFLTFVFKVLEFACVPPTYEYCHGMACFANVSLIIGMLTAIIGDLASHFECITIG 778
Db 769 PSCFDYVMHFLTFVFKVLEFACVPPTYEYCHGMACFANVSLIIGMLTAIIGDLASHFECITIG 828
Oy 779 LKDSYTAAYFAVAGTSVPPTFASKAALADYADASIGNVTSNNAVNFGLGILANVAA 838
Db 839 LKDSYTAAYFAVAGTSVPPTFASKAALADYADASIGNVTSNNAVNFGLGILANVAA 888
Oy 839 IYMALOGOEHFHAGTAFSVTLTFEAFVCSIVLLYRRRPHLGGELGPRCKLATITML 898
Db 888 IYHANGDEQFKVSPGLTAFSVTLTFEAFVCSIVLLYRRRPHLGGELGPRCKLATITML 948
Oy 899 FVSLMLYLTFATLEAYCYIKGF 921
Db 949 FVSLMLYLTFATLEAYCYIKGF 971

RESULT 10
A54139
Nat/Ca2+-exchanging protein NCX2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 18-Aug-2000
C:Accession: A54139
R.L.L., Z.: Matsuda, S.: Hryshko, L.V.: Nicoli, D.A.: Bersohn, M.M.: Burke, E.P.: Lifton, J. Biol. Chem. 269, 17434-17439, 1994
A:Title: Cloning of the NCX2 isoform of the plasma membrane Na(+)-Ca(2+) exchanger.

A:Reference number: A54139; MUID:94292496; PMID:8021246
A:Accession: A54139
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-921 <L1>
A:Cross-references: GB:008141; MID:9511680; PIDN:AAA19920.1; PID:9511681
C:Superfamily: human Na+/Ca2+-exchanging protein
C:Keywords: transmembrane protein

Query Match 70.0%; Score 3357; DB 2; Length 921;
Best Local Similarity 69.6%; Pred. No. 9, 6e-218;
Matches 635; Conservative 130; Mismatches 114; Indels 34; Gaps 9;

Oy 31 EAGSGSDVPSIQONNE-----SCSGSDCKEYVILPIWPEKPSGDKIARATYFVALI 85
Db 21 EATPTPLPPPPANDSDASPGGCGQSYRQPGVLLVWPEBDDPSLGDKAARAVYFVAAY 80
Oy 86 YMFGLGSIADRFMAISIEYTSQEREVITKRNGETSTTIRVNETYSNLTLMALGSSA 145
Db 81 YMFGLGSIADRFMAISIEYTSQEREVITKRNGETSVGTIRVNETYSNLTLMALGSSA 140
Oy 146 PELLSLIEVCGHGFACGLGPGSTTVGSAAFNMFIIGICVYVVPDGETRIKHLRVFPI 205
Db 141 PELLSLIEVCGHGFACGLGPGSTTVGSAAFNMFIYVAVCYVYIPAGESRKIKHLRVFPI 200
Oy 206 TAAVSFAITIMLYMLTAVSPGVOWEGLLTFEPFVOLLAMADKRLTFYKMHKKY 265
Db 201 TAAVSFAITIMLYMLTAVSPGVOWEGLLTFEPFVOLLAMADKRLTFYKMHKKY 260
Oy 266 PRDKHNGIIEEGDHPKGIEMDGKMMNHFLDGNL---VPLEGKEVDESREMRITL 320
Db 261 PRDKHNGIIEEGDHPKGIEMDGKMMNHFLDGNL---VPLEGKEVDESREMRITL 319
Oy 321 KDLQKHPKEDLDLVEMANYALS HQKRAFRIOATMMTGAGNLLKKAHAEQAKKA 380
Db 320 KDLQKHPKEDLDLVEMANYALS HQKRAFRIOATMMTGAGNLLKKAHAEQAKKA 379
Oy 381 SSMSEVHTDEPDTFSKVPFDPGSYOCLENCGAVLLTVYRKGGDSKTMVDYKTEGSA 440
Db 380 GA-NDGAPDEDEDGASRIPEPSLYHCLNCSVLLSVAQGGEGNSTYVYDRIEDGSA 438
Oy 441 NAGADVEFTGTVLKPGETQKEFSVGIIDDDIFEEDEHFYRLSNVRIEEOPE---PEE 496
Db 439 KAGSDVESEGLTVFPRGTOKELRIGIIDDIFEEDEHFYRLSNVRIEEOPE---PEE 498
Oy 497 GMPALFNSPLPRVAVLPCVATVTIIDDHAGITFECDTIHSESIGVMEVKVLRYS 556
Db 499 G-----GRPKGRVAPLTLATVITLDDHAGITFECDTIHSESIGVMEVKVLRYS 549
Oy 557 GARGTVTFPRFVEGAKSGGEDEFTYGELEKKNDETVKTRVKIVDEEYERQENFPT 616
Db 550 GARGTVTFPRFVEGAKSGGEDEFTYGELEKKNDETVKTRVKIVDEEYERQENFPT 609
Oy 617 ALGEPKMMERGISDVT-----DRKLTMEDEBKRIAEKGRPVLGHPKLEVIIEESYEF 670
Db 610 ELGQPMKLRGISALLNNGDDGRKLTAEERQRIAEKGRPVLGHPKLEVIIEESYEF 669
Oy 671 KTTVDKLIKTNLALVYTHSMRQDEMEATVTSAAGEDDESEG---EERLPSCFDYVMHF 728
Db 670 KTTVDKLIKTNLALVYTHSMRQDEMEATVTSAAGEDDESEG---EERLPSCFDYVMHF 728
Oy 729 LTFVFKVLEFACVPPTYEYCHGMACFANVSLIIGMLTAIIGDLASHFECITIGLDSYAVVF 788
Db 729 LTFVFKVLEFACVPPTYEYCHGMACFANVSLIIGMLTAIIGDLASHFECITIGLDSYAVVF 788
Oy 789 VAFGTSVPPTFASKAALADYADASIGNVTSNNAVNFGLGILANVAAIYMALOGOEF 848
Db 789 VAFGTSVPPTFASKAALADYADASIGNVTSNNAVNFGLGILANVAAIYMALOGOEF 848
Oy 849 HVSAGTAFSVTLTFEAFVCSIVLLYRRRPHLGGELGPRCKLATITMLFVSLMLYL 908
Db 849 EVRTGTLARSVTLTFEAFVCSIVLLYRRRPHLGGELGPRCKLATITMLFVSLMLYL 908

QY 909 FATLEAYCIKGF 921
 DB 909 FATLEAYCHIRGF 921

RESULT 11

B89047

Protein C10G8.5 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001

C:Accession: B89047

R:Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; PMID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C_eleg

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: B89047

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-890 <STO>

A:Cross-references: GB:chr_V; PIDN:AAB09172.1; PID:g1572830; GSPDB:GN00023; CESP:C10G8.5

Genetics:

A:Gene: C10G8.5

A:Map position: 5

C:Superfamily: human Na⁺/Ca²⁺-exchanging protein

Query Match 41.8%; Score 2007; DB 2; Length 890;

Best Local Similarity 45.9%; Pred. No. 6.8e-127;

Matches 416; Conservative 145; Mismatches 232; Indels 114; Gaps 13;

QY 87 MFLGVSIADRFMASIEVITSOEREYIKRPNGESTTTIRVWNETVSNLTLMALGSSAP 146

DB 1 MFLGISIVADRFMSIEVITSMERTIVYKRPGLDPMAYVRIMNDIVSNLTLMALGSSAP 60

QY 147 ELLLSIEVCGHGFIADDLSPSTIVGSAFNMFTIIGICVYVPPDGTGRIKILRVFPT 206

DB 61 ELLLSIEVARGFEADLDPMITIVGSAFNMFTIIGICVYVPPDGTGRIKILRVFPT 120

QY 207 AANSIFAYILWYMLIAVSPGVVWEGLLTLPFFPVCLIAVADKRLIEFYKMHKKYR 266

DB 121 AIMSVPFVWVLLYLAFFSGEIEIMGALTFEPPLTVTAATADIKLQNKFLPHRYR 180

QY 267 TDKRGIIETEGDHPKGIEMDKMNSHFLDGNLVPLEGEVDESREMIIRILKDKQ 326

DB 181 RGSN-GQMINTAEEMKMLE-----NGTQGPALKAFEEHNGEFLREIRKQ 228

QY 327 HPEKDLQVEMANYTALSHQOKSRAFYRQATRMATGACNILLKHAADQAKKA-SSMSE 365

DB 229 NPHTTPELQKQAEYEMISRGPKSRAFYRQATRRRLIGGDIVYKRIKIDKHNKALDALVQ 288

QY 386 VHRDEPDEFTSKYFDFCSYQCLENGAVLLTVYRKGGDKMTYVYDTEEDGSANAGAD 445

DB 289 AOEQSDNCKTKFLPDRAHTTVLESFVYVGRDGGPGLTVMVYDFEDGSANAGSD 348

QY 446 YEFTEGTIVLKPGETOKESFVGIIIDDFEDEFHEFVRLSNVRIEEDQPEG--MPPAIF 503

DB 349 YIPKKGTLFTEYEDKHQKVTIEVVDVDFEDEFHEFVRLCNLRY--RTKDGIIDPTRI 405

QY 504 NSLPLPAVLAAPCVATVTLDDDHAGITFEEDCTIVSSSIGVMEKVLVTSARCTVI 563

DB 406 GGLPV--AQLEMPATATIMLDDHAGVFGFEDHDFQVENCGLSLQMKRHSASARKVI 463

QY 564 VPFEFTGATGGGEDEFDYGELEFNDKTVTKIRKVIYDEDEYEQENFTALGSPKK 623

DB 464 IIPRTVGTGA-SADKHEEMKEGELVEFDNOTBALVEIGIVDTQEYSDVFIETLSPTW 522

QY 624 -----MERGISDVTDRK-----LTMBEEA 643

DB 523 AKKMDLSRIQERFORMERKRGSSVASSEKSDSTENALAPAEKSTRAASVDLQPSDP 582

QY 644 KR-----IAEMGKPVLGCHPKL 660

DB 583 RRSQNTSPHLTSFRNRRLGSMIAGMKGGNGDEVTTLSPSOLEIAEMGKPRLGFTTC 642

QY 661 EVLIEESEYEKFTVVDKLIKRTNLTALVYGTSHMRDQEMEAITVASAGDEDED---ESGEE 716

DB 643 QITRESKEFGQIVDRKIKNANTRIMGTSHMRDQEMEAITVASAGDDDDDEGEDGE 702

QY 717 R---LPSCFDYVMHFLTVEMKVLVACVPPTREYCHGMACFVSLIIGMTAIGDLASHF 773

DB 703 KEPEEPCCMDYVMHVLTVPMKLTFAFATIPPDYFGMATFVAALFMIGVLTAVVGDLASQF 762

QY 774 GCTTGLKDSYAVYFAVFGSVSDTFRASKAALQDYADASIGNVYCSNANVNFGLIGLA 833

DB 763 GCWVGAKDAVTAISFVALGTSVSDTFRASKVSAVDKTDADNAVGNVSNVNFGLIGLA 822

QY 834 MSVAATYMAIQQGGEFHSAGTLAFSVTLFTFAFVCISVLYRRRPHLGGELGSPRCCKL 893

DB 823 WSNAAITYHMGGKRLVLPDNGLSFVILFCTEAVLCITIVLARNKKVGGELGSPRLALR 882

QY 894 ATTWLFV 900

DB 883 T---IFV 886

RESULT 12

T24110

hypoetical protein ZC168.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C:Accession: T24110; T27507

R:Berk's, M.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z19841

A:Accession: T24110

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-807 <MIL>

A:Cross-references: EMBL:Z70309; PIDN:CAA94363.1; GSPDB:GN00022; CESP:ZC168.1

A:Experimental source: clone R102

R:Berk's, M.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z20378

A:Accession: T27507

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-807 <MIL>

A:Cross-references: EMBL:Z70312; PIDN:CAA94387.1; GSPDB:GN00022; CESP:ZC168.1

A:Experimental source: clone ZC168

C:Genetics:

A:Gene: ZC168.1

A:Map position: 4

A:Introns: 38/1; 177/3; 346/1; 365/1; 369/3; 414/3; 455/3; 692/3; 743/2

Query Match 24.8%; Score 1192; DB 2; Length 807;

Best Local Similarity 33.6%; Pred. No. 4.3e-72;

Matches 302; Conservative 150; Mismatches 320; Indels 126; Gaps 20;

QY 47 SCGSSSDCKEGLIPIYPPNPSSLGDKIARIVYFVALIMFGVSTIADRFMASIEVIT 106

DB 2 SSSANLCKNGKILL-----PALETPRNAIILYIAGLFCFGLGIAIAADIFMCSIEQIT 54

QY 107 SQREYVITKRPNGESTTT-----IRVWNETVSNLTLMALGSSAPEILLSLIEV 155

DB 55 SATRKVKYQKQKAGOLVAKEDEDEIDQYDVYRIMNPVANTLMALGSSAPEILLSTIEI 114

QY 156 CGGCTIAGDGPSTIVGSAFNMFTIIGICVYVPPDGTGRIKILRVFPTAAMSTFAYI 215

DB 115 VGNQFAGDGPSTIVGSAFNMFTIIGICVYVPPDGTGRIKILRVFPTAAMSTFAYI 173

QY 216 WLYMILAVFSPGVVWEGLLTLPFFPVCLIAVADKRLIEFYKMHKKYRTD-----268

DB 174 WFLVLYVITPNVVDWEALITLIFLILVYVSYADAQI-----WKKKSSDLOELEM 228

QY 269 -KHRGIIETEGDHPKGIEMDKMNSHFL--DGNLVPLEGEVDESREMIIRILKDL 323

Db 229 AOHGKV-----DDQPEKLSDEIKKMASNLSLNKEENDVIATPSPVDIVR-----RWTSI 280
Qy 324 KOKHPEKLDOLVEMANYALSHOOKSRAFRIOATRMATGAGNLLKHAADQAKKASSM 383
Db 281 SHYTPSLDEDOAKILAVRSRTMSHRLYYRIRAIRQLSSS--WRKSEEEVLMKMNQ 337
Qy 384 SEVHTDEPEDFISKVEFPDPCSYOCLENCAGVLLTVVRKGGMSKTMVYDTETEDSANAG 443
Db 338 ES--TDSASRRKTYEFERARVYRDATDEYSLKTERK-GNWSKFTYSTATVNLAKD 394
Qy 444 ADETECTVVLKRGCTOKESVGIIDDDIFEEDHFVRLSNVRIEEOPEEGMPAIF 503
Db 395 LNFLEKSTLOFNPGLKTKISIQILNANMRPNDFVHLKIQOVDD-----443
Qy 504 NSLPLRAVLASPCVAVTITDDHAGIFTECDTIH-VSESIGVMEKVLRTSG-ARGT 561
Db 444 -----SKICGA-----CNVAHVYKKNAGFSRSFVTRRGKLLKP 478
Qy 562 VIVPRTEGTAAGGGEDEFTYGELEKNDETVTKIVYDEEYERQENFTALGEP 621
Db 479 LQVHETEDVAKOGDDTTAVKDGILGEGGEYKEYIDIVIDMDKDEAFIEL--L 536
Qy 622 KMERGISDVTDRKLTMEEBEAKRIAEMGKPVLCGEHPKLEVIIESEYEFK--TVYDKLIK 679
Db 537 KYDEGVSIGTRRKATI-----TIISDNVKNKTINVRKLMG 573
Qy 680 KTNLALVGVTHSMRDQMEAITVSAGDEDESGEERLPSCFDYVHFLTVFKVLPAC 739
Db 574 HYMRQLRGKATWKEOILNAVSVNA-----GDLNANVYSDCILHALFPFMAFAF 624
Qy 740 VPPEYCGMACFANVILIGLTAIGLASHFGCTIGLSDVTAVVFAVFGTSVPPTF 799
Db 635 LPPPIFGYCFYVALVIGLTVAVGVDSIFECMGGLDAVATRLVALGTSLPDTF 684
Qy 800 ASKAAALODVYADASIGNVTSNANVFLGIGLANSVAIYALOGQEFHSAGTLAFSV 859
Db 685 ASKIAESDPTADNANVGVTSNSVNFVLGILPVIASLVWASGSEFRDAGDLGFSV 744
Qy 860 TLFITFAVCISVLLYRRRPHL--GGEIGGRGCKLATTWLVSLMLYLIFATLEAY 915
Db 745 TVFMICSVLFLVVLVLRKRLKAFGOGELGPGPTKLSALFEFVGLIYVGLSIWKMY 802

RESULT 13
152640
cardiac sodium/calcium exchanger, cerebellar granule neurons - rat (fragment)
C:Species: Rattus sp. (rat)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 18-Aug-2000
C:Accession: 152640
R:Marlier, L.N.; Zheng, T.; Tang, J.; Grayson, D.R.
Brain Res. Mol. Brain Res. 20, 21-39, 1993
A:Title: Regional distribution in the rat central nervous system of a mRNA encoding a pc
A:Reference number: 152640; MUID:94077033; PMID:8255180
A:Accession: 152640
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-152 <RES>
A:Cross-references: GB:S6769; NID:9459304
C:Superfamily: human Na+/Ca2+-exchanging protein
C:Keywords: cardiac muscle; heart

Query Match 13.7%; Score 659; DB 2; Length 152;
Best Local Similarity 82.9%; Pred. No. 3e-37;
Matches 126; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 700 ITVSAGDEDESGEERLPSCFDYVHFLTVFKVLFACVPTFYCGMNAFAVSIIT 759
Db 1 ITVSAGDEDDDECEERLPSCFDYVHFLTVFKVLFAPFPPTFYKMGMACTIYSLMT 60
Qy 760 GMLTAIIGDLASHFGCTIGLSDVTAVVFAVFGTSVPPTFASKAALODVYADASIGNVT 819
Db 61 GLTFATIGDLASHFGCTIGLSDVTAVVFAVFGTSVPPTFASKAALODVYADASIGNVT 120

Qy 820 GSNANVFLGIGLANSVAIYALOGQEFHS 851
Db 121 GSNANVFLGIGLANSVAIYALOGQEFHS 152

RESULT 14
T00424
probable Na+/Ca2+ antiporter [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T30822.10
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C:Accession: T00424; C84917
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; M
submitted to the EMBL Data Library, October 1998
A:Description: Arabidopsis thaliana chromosome II BAC T30822 genomic sequence.
A:Reference number: 21419
A:Accession: T00424
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-538 <ROU>
A:Cross-references: EMBL:AC002535; NID:93529657; PID:93522931
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Unayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C84917
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-538 <STO>
A:Cross-references: GB:AE002093; NID:93522931; PID:NAC62871.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g47600; T30B22.10
A:Map position: 2
A:Introns: 131/1; 189/3; 229/2; 287/1; 333/1; 397/1; 440/2

Query Match 12.0%; Score 573.5; DB 2; Length 538;
Best Local Similarity 22.2%; Pred. No. 1e-30;
Matches 191; Conservative 107; Mismatches 195; Indels 369; Gaps 22;

Qy 64 YPENSLDKIARVYVVALIYMFGLVSIADRFMASIEVTSQREVTIKKPGKST 123
Db 29 FPGENTLSDGL-RGVLYFLGLAYCFGLSATARFFKSMENVVKSRKRVVTIDPTKAEV 87
Qy 124 TTI-RVWNETVSNLTMLAGSAPRILSLIEV--CGHGTAGDLPSTVGSAAFNMF 179
Db 88 IYKKVWNTIADISLLAFGTSFPOISLATIDAINNGERY-AGGLGCTLVGSAFPLDF 146
Qy 180 IITGICVYVDPDETRKIKHLVFEFTAMSIFAVIMYLMLAVSPGVQVWVEGLTLF 239
Db 147 PTHAVCVVPRKAGELKISDLGVMLVLEWSPWAIWYIILIEVWSPVITLVEALLTVL 206
Qy 240 FFRVCVLLANVADKRLLYKKYKHKYRDKKHGIIIEBGRPKIEMDKMNSHFLDG 299
Db 207 OYGLLVHAHYADKR--WPLYL-----LPMRGDRP-----236
Qy 300 NLVPLEGKEVDSESRERIRILDKQKHPKEDLDQLVEMANYALSHOOKSRAFYRIOT 359
Db 237 EWPV--EIDTSK-----DDNDND-----253
Qy 360 RMTGTAGNLLKHAADQAKKASSMSEVHTDEPEDFISKVEFPDPCSYOCLENCAGVLLTVV 419
Db 254 -----VHDVYSDAODAV-----266
Qy 420 RKGGMSKTMVYDYKTEDEGSANAGADYFETBETVVLKRGCTOKESVGIIDDDIFEEDEN 479
Db 267 -----ESGSRN-----IVD-----275
Qy 480 FVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVAVTITDDHAGIFTECDTI 539

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Db 276 -----If-----SI 279
Qy 540 HVSESIGMEVKLRTSGARCTIVPRRYEGNAKGGGDEEDTGYGLEKKNDETAKTIR 5999
Db 280 H-----SANNDGTITHTVADPP-----DSATKKGK 306
Qy 600 VKIVDEEYERQENPFIALGEPKMMERGISDVTDRKLTMBEBAKRIAEMGPVILGHPK 6599
Db 307 AK-----308
Qy 660 LEVIIIESEYERKTYDKLIKKTNLALVGTSHWDEQFMEAITVSAADEDEDESGEERLP 719
Db 309 -----NSTVFDI-----MKHQVDIAITVKIF-----NLP 332
Qy 720 SCDFDY-----MHPLVYEMKVLVFCAPPPTTEYCHGACAFVSLIITMLTAIIGDLASHF 773
Db 333 MDSTIYLRIAKSEFMHLLAPMKLLFAFPPCNIAHGMWIAFTCSLELFIISGAVFYVTRFTDLI 392
Qy 774 GCTIGLKDSVAAYVFAVFGTSVPTPEFVSKAAALODVADASIGNVTGSNNVNFVLTIGLA 833
Db 393 SCVGININRYVIALFALALASGTSMPDLVASKIAEAEQOLADASNAIANITTSNSVNITVIGICVP 452
Qy 834 WSVAAI--YMAALQOEHFVSAAGTLAFSVLTETTFPAFVCSISVLLYRRRPHUGELGEGRCG 891
Db 453 WLINTVNYFYRREPLVIEENKAGSFLLETFEATSVGCIYVLVRLR--TIGAELEGGRWM 511
Qy 892 KLATTMLVFSIMLXILFATIE 913
Db 512 AMUTSAFEMMLAVVEFVYLSLAK 533

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